L18: Entry 4 of 5 File: USPT Apr 14, 1998

US-PAT-NO: 5739008
DOCUMENT-IDENTIFIER: US 5739008 A

TITLE: DNA encoding a protein comprising calmodulin-and actin-binding human caldesmon peptide fragment

DATE-ISSUED: April 14, 1998

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Hayashi; Ken'ichiro	Takatsuki			JP
Hashida; Takashi	Otsu			JP
Asada; Kiyozo	Shiga-ken			JP
Kotani; Hirokazu	Moriyama			JP
Kato; Ikunoshin	Uji			JP
Sobue; Kenji	Ibaraki-shi, Osaka-fu			JP

US-CL-CURRENT: 435/69.1; 435/320.1, 435/325, 530/350, 536/23.4, 536/23.5, 536/24.31

CLAIMS:

What we claim is:

1. An isolated DNA encoding an actin- or calmodulin-binding polypeptide fragment of a human caldesmon protein, said DNA comprising a nucleotide sequence encoding at least the amino acid sequence shown in SEQ ID NO:1, wherein said caldesmon protein has the amino acid sequence shown in SEQ ID NO:5 or SEQ ID NO:6.

2. The DNA according to claim 1, comprising a nucleotide sequence encoding the amino acid sequence shown in SEQ ID NO:2, SEQ ID NO:3 or SEQ ID NO:4.

3. The DNA according to claim 1, which comprises the nucleotide sequence shown in SEQ ID NO:7.

4. The DNA according to claim 1, which comprises a nucleotide sequence selected from the group consisting of SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9 and SEQ ID NO:10.

5. An isolated DNA which is complementary to the DNA according to any one of claims 1, 2, 3, or 4.

6. An isolated DNA which hybridizes under stringent conditions with the complement of the DNA according to any one of claims 1, 2, 3 or 4, said DNA coding for a human polypeptide that has calmodulin-binding activity and actin-binding activity.

7. An isolated DNA encoding a chimeric protein, comprising the DNA according to any one of claims 1, 2, 3, or 4.

8. A cDNA which codes for a human caldesmon protein having the amino acid sequence shown in SEQ ID NO:5 or SEQ ID NO:6.

9. The cDNA according to claim 8, which has a nucleotide sequence shown in SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13 or SEQ ID NO:14.

10. A recombinant vector comprising the DNA according to any one of claims 1, 2, 3, 4 or 7 or the cDNA according to any one of claims 8 or 9.

11. A host cell transformed with the recombinant vector according to claim 10.

12. A process for producing a human caldesmon protein or active fragment thereof, which comprises:

culturing the host cell according to claim 11 under conditions to express the human caldesmon protein or active fragment thereof, and

isolating the caldesmon protein or active fragment.

Previous Doc Next Doc Go to Doc#

Refine Search

Search Results -

Terms	Documents
dna encoding actin	5

Database:
US Pre-Grant Publication Full-Text Database
US Patents Full-Text Database
US OCR Full-Text Database
EPO Abstracts Database
JPO Abstracts Database
Derwent World Patents Index
IBM Technical Disclosure Bulletins

Search: L18

Refine Search

Recall Text | Clear | Interrupt

Search History

DATE: Friday, August 18, 2006 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT; PLUR=YES; OP=ADJ			
L18	dna encoding actin	5	L18
L17	cdna encoding actin	4	L17
L16	actin with cdna	1237	L16
L15	actin with polynucleotide with encoding	7	L15
DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=ADJ			
L14	(L13 or l12 or l11) and l5	1	L14
L13	asada-masanori.in.	49	L13
L12	osaka-kenji.in.	37	L12
L11	osaka-kenji-irie.in.	0	L11
L10	takai-yoshimi.in.	43	L10
L9	(l6 or l7 or l8) and l5	3	L9
L8	afadin	30	L8
L7	ALPHA-ACTININ-2	16	L7
L6	ALPHA-ACTININ-1	6	L6

L5	AFADIN DIL DOMAIN-BINDING PROTEIN OR ADIP	2078	L5
DB=USPT; PLUR=YES; OP=ADJ			
L4	L3 and (produc$ with (polypeptide or protein))	1	L4
L3	L2 and vector	1	L3
L2	L1 and host cell	1	L2
L1	6943241.pn.	1	L1

END OF SEARCH HISTORY

Freeform Search

Database: US Pre-Grant Publication Full-Text Database
US Patents Full-Text Database
US OCR Full-Text Database
EPO Abstracts Database
JPO Abstracts Database
Derwent World Patents Index
IBM Technical Disclosure Bulletins

Term: (L13 or l12 or l11) and l5

Display: 10 **Documents in Display Format:** CIT **Starting with Number** 1

Generate: ○ **Hit List** ◉ **Hit Count** ○ **Side by Side** ○ **Image**

Search Clear Interrupt

Search History

DATE: Friday, August 18, 2006 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=ADJ			
L14	(L13 or l12 or l11) and l5	1	L14
L13	asada-masanori.in.	49	L13
L12	osaka-kenji.in.	37	L12
L11	osaka-kenji-irie.in.	0	L11
L10	takai-yoshimi.in.	43	L10
L9	(l6 or l7 or l8) and l5	3	L9
L8	afadin	30	L8
L7	ALPHA-ACTININ-2	16	L7
L6	ALPHA-ACTININ-1	6	L6
L5	AFADIN DIL DOMAIN-BINDING PROTEIN OR ADIP	2078	L5
DB=USPT; PLUR=YES; OP=ADJ			
L4	L3 and (produc$ with (polypeptide or protein))	1	L4
L3	L2 and vector	1	L3
L2	L1 and host cell	1	L2
L1	6943241.pn.	1	L1

END OF SEARCH HISTORY

Refine Search

Search Results -

Terms	Documents
(L13 or L12 or L11) and L5	1

Database: US Pre-Grant Publication Full-Text Database; US Patents Full-Text Database; US OCR Full-Text Database; EPO Abstracts Database; JPO Abstracts Database; Derwent World Patents Index; IBM Technical Disclosure Bulletins

Search: L14

Refine Search | Recall Text | Clear | Interrupt

Search History

DATE: Friday, August 18, 2006 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=ADJ			
L14	(L13 or l12 or l11) and l5	1	L14
L13	asada-masanori.in.	49	L13
L12	osaka-kenji.in.	37	L12
L11	osaka-kenji-irie.in.	0	L11
L10	takai-yoshimi.in.	43	L10
L9	(l6 or l7 or l8) and l5	3	L9
L8	afadin	30	L8
L7	ALPHA-ACTININ-2	16	L7
L6	ALPHA-ACTININ-1	6	L6
L5	AFADIN DIL DOMAIN-BINDING PROTEIN OR ADIP	2078	L5
DB=USPT; PLUR=YES; OP=ADJ			
L4	L3 and (produc$ with (polypeptide or protein))	1	L4
L3	L2 and vector	1	L3
L2	L1 and host cell	1	L2

L1	6943241.pn.	1	L1

END OF SEARCH HISTORY

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=> s afadin dil domain-binding protein or adip#
L1 900 AFADIN DIL DOMAIN-BINDING PROTEIN OR ADIP#

=> s l1 and (alpha-actinin-1 or alpha-actinin-2 or actinin# or afadin#)
5 FILES SEARCHED...
L2 19 L1 AND (ALPHA-ACTININ-1 OR ALPHA-ACTININ-2 OR ACTININ# OR AFADIN#)

=> dup rem l2
PROCESSING COMPLETED FOR L2
L3 5 DUP REM L2 (14 DUPLICATES REMOVED)

=> d ibib abs l3 1-5

L3 ANSWER 1 OF 5 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN DUPLICATE 1
ACCESSION NUMBER: 2004-404616 [38] WPIDS
DOC. NO. NON-CPI: N2004-322275
DOC. NO. CPI: C2004-152052
TITLE: New polynucleotide encoding an ***afadin*** dilution domain binding protein having avidity with ***afadin*** or ***actinin*** , useful for diagnosing heart diseases e.g. myocardial infarction.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): ASADA, M; IRIE, K; TAKAI, Y
PATENT ASSIGNEE(S): (EISA) EISAI CO LTD; (ASAD-I) ASADA M; (IRIE-I) IRIE K; (TAKA-I) TAKAI Y
COUNTRY COUNT: 2
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
JP 2004135658	A	20040513	(200438)*		37
US 2006160092	A1	20060720	(200648)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
JP 2004135658	A	JP 2003-293554	20030814
US 2006160092	A1	US 2003-644084	20030820

PRIORITY APPLN. INFO: JP 2002-284263 20020927
AN 2004-404616 [38] WPIDS
AB JP2004135658 A UPAB: 20040616
NOVELTY - A polynucleotide (I) encoding an ***afadin*** dilution domain binding protein having avidity with ***afadin*** / ***actinin*** , comprises a sequence (S1) of 2692 or 3195 nucleotides,

given in specification or a sequence which hybridizes with (S1), or encodes a protein having a sequence (S2) of 615 or 613 amino acids, given in specification or a sequence which has alterations in amino acid(s) of (S2), is new.

DETAILED DESCRIPTION - A polynucleotide (I) encoding ***afadin*** dilution domain binding protein (***ADIP***) having avidity with ***afadin*** or ***actinin*** , comprises a fully defined sequence (S1) of 2692 or 3195 nucleotides as given in the specification or a sequence which hybridizes under stringent conditions with (S1), or encodes protein having a fully defined sequence (S2) of 615 or 613 amino acids as given in the specification or a sequence which has substitution, deletion, insertion and/or addition in one or more amino acid(s) of (S2).

INDEPENDENT CLAIMS are included for the following:

(1) a polypeptide (II) encoded by (I);

(2) a vector (III) comprising (I);

(3) a host cell (IV) comprising (I) or (III);

(4) a polynucleotide having at least 15 nucleotides, hybridizes specifically under stringent condition with (I);

(5) a polynucleotide or the antisense polynucleotide with respect to one part of (I); and

(6) an antibody binding with (II).

ACTIVITY - Cardiant.

MECHANISM OF ACTION - ***Afadin*** binding inhibitor; ***Actinin*** binding inhibitor.

USE - (I) or (II) is useful for diagnosing heart disease such as myocardial infarction or myocarditis which involves (a) detecting the expression level of (I) that encodes (II) in a subject, (b) preparing a RNA sample from the cardiac myocyte of a subject, measuring the quantity of RNA contained in RNA sample, and comparing the quantity of the measured RNA with a control, or (c) preparing a protein sample from the cardiac myocyte of a subject, measuring the quantity of (II) contained in the protein sample, and comparing the quantity of the measured polypeptide with a control. (II) is useful for the screening a candidate compound as the medical agent for controlling an actin structure which involves contacting ***afadin*** or ***actinin*** , (II) and the test compound, measuring the avidity of ***afadin*** or an ***actinin*** and (II), and selecting the compound to which the avidity is changed by comparing it with the control, where a test compound is not made to contact. (IV) is useful for producing (II) which involves culturing (IV), and collecting the produced (II) from the host cell or its culture supernatant (all claimed). (II) is useful for screening a therapeutic agent for treating heart disease.

ADVANTAGE - (I) is efficient in diagnosing heart disease and screening a candidate compound as medical agent for treating heart disease.

Dwg.0/10

L3 ANSWER 2 OF 5 MEDLINE on STN DUPLICATE 2

ACCESSION NUMBER: 2004425875 MEDLINE <<LOGINID::20060818>>

DOCUMENT NUMBER: PubMed ID: 15330861

TITLE: Requirement of the actin cytoskeleton for the association of nectins with other cell adhesion molecules at adherens and tight junctions in MDCK cells.

AUTHOR: Yamada Akio; Irie Kenji; Fukuhara Atsunori; Ooshio Takako; Takai Yoshimi

CORPORATE SOURCE: Department of Molecular Biology and Biochemistry, Osaka University Graduate School of Medicine/Faculty of Medicine, Suita 565-0871, Japan.

SOURCE: Genes to cells : devoted to molecular & cellular mechanisms, (2004 Sep) Vol. 9, No. 9, pp. 843-55. Journal code: 9607379. ISSN: 1356-9597.

PUB. COUNTRY: England: United Kingdom

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200410

ENTRY DATE: Entered STN: 28 Aug 2004
Last Updated on STN: 19 Oct 2004
Entered Medline: 18 Oct 2004

AB Nectins, Ca(2+)-independent immunoglobulin-like cell adhesion molecules (CAMs), first form cell-cell adhesion where cadherins are recruited, forming adherens junctions (AJs) in epithelial cells and fibroblasts. In

addition, nectins recruit claudins, occludin, and junctional adhesion molecules (JAMs) to the apical side of AJs, forming tight junctions (TJs) in epithelial cells. Nectins are associated with these CAMs through peripheral membrane proteins (PMPs), many of which are actin filament-binding proteins. We examined here the roles of the actin cytoskeleton in the association of nectins with other CAMs in MDCK cells stably expressing exogenous nectin-1. The nectin-1-based cell-cell adhesion was formed and maintained irrespective of the presence and absence of the actin filament-disrupting agents, such as cytochalasin D and latrunculin A. In the presence of these agents, only ***afadin*** remained at the nectin-1-based cell-cell adhesion sites, whereas E-cadherin and other PMPs at AJs, alpha-catenin, beta-catenin, vinculin, alpha- ***actinin*** , ***ADIP*** , and LMO7, were not concentrated there. The CAMs at TJs, claudin-1, occludin and JAM-1, or the PMPs at TJs, ZO-1 and MAGI-1, were not concentrated there, either. These results indicate that the actin cytoskeleton is required for the association of the nectin- ***afadin*** unit with other CAMs and PMPs at AJs and TJs.

L3 ANSWER 3 OF 5 MEDLINE on STN DUPLICATE 3
ACCESSION NUMBER: 2004451971 MEDLINE <<LOGINID::20060818>>
DOCUMENT NUMBER: PubMed ID: 15358183
TITLE: ***Afadin*** - and alpha- ***actinin*** -binding protein ***ADIP*** directly binds beta'-COP, a subunit of the coatomer complex.
AUTHOR: Asada Masanori; Irie Kenji; Yamada Akio; Takai Yoshimi
CORPORATE SOURCE: Department of Molecular Biology and Biochemistry, Osaka University Graduate School of Medicine/Faculty of Medicine, Suita 565-0871, Japan.
SOURCE: Biochemical and biophysical research communications, (2004 Aug 20) Vol. 321, No. 2, pp. 350-4.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200410
ENTRY DATE: Entered STN: 14 Sep 2004
Last Updated on STN: 7 Oct 2004
Entered Medline: 6 Oct 2004
AB ***Afadin*** DIL domain-interacting protein (***ADIP***) is a novel protein that binds both ***afadin*** and alpha- ***actinin*** and localizes at adherens junctions, which are formed by nectins and cadherins, cell-cell adhesion molecules. ***Afadin*** is an actin filament (F-actin)-binding protein which connects nectins to the actin cytoskeleton. alpha- ***Actinin*** is another F-actin-binding protein that is indirectly associated with cadherins through the catenin complex. ***ADIP*** is at least partly involved in the physical association of nectins and cadherins. We show here that ***ADIP*** furthermore binds beta'-COP, a subunit of the coatomer complex. ***ADIP*** co-localizes with beta'-COP at the Golgi complex in Madin Darby canine kidney and normal rat kidney cells. These results suggest that ***ADIP*** is involved in vesicle trafficking from the Golgi to the endoplasmic reticulum and through the Golgi complex by interacting with the coatomer complex.

L3 ANSWER 4 OF 5 MEDLINE on STN DUPLICATE 4
ACCESSION NUMBER: 2003053398 MEDLINE <<LOGINID::20060818>>
DOCUMENT NUMBER: PubMed ID: 12446711
TITLE: ***ADIP*** , a novel ***Afadin*** - and alpha- ***actinin*** -binding protein localized at cell-cell adherens junctions.
AUTHOR: Asada Masanori; Irie Kenji; Morimoto Koji; Yamada Akio; Ikeda Wataru; Takeuchi Masakazu; Takai Yoshimi
CORPORATE SOURCE: Department of Molecular Biology and Biochemistry, Osaka University Graduate School of Medicine/ Faculty of Medicine, Suita 565-0871, Japan.
SOURCE: The Journal of biological chemistry, (2003 Feb 7) Vol. 278, No. 6, pp. 4103-11. Electronic Publication: 2002-11-21.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English

FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF532969; GENBANK-AF532970
ENTRY MONTH: 200303
ENTRY DATE: Entered STN: 4 Feb 2003
Last Updated on STN: 22 Mar 2003
Entered Medline: 21 Mar 2003

AB ***Afadin*** is an actin filament (F-actin)-binding protein that is associated with the cytoplasmic tail of nectin, a Ca(2+)-independent immunoglobulin-like cell-cell adhesion molecule. Nectin and ***afadin*** strictly localize at cell-cell adherens junctions (AJs) undercoated with F-actin bundles and are involved in the formation of AJs in cooperation with E-cadherin in epithelial cells. In epithelial cells of ***afadin*** (-/-) mice and (-/-) embryoid bodies, the proper organization of AJs is markedly impaired. However, the molecular mechanism of how the nectin- ***afadin*** system is associated with the E-cadherin-catenin system or functions in the formation of AJs has not yet been fully understood. Here we identified a novel ***afadin*** -binding protein, named ***ADIP*** (***afadin*** DIL domain-interacting protein). ***ADIP*** consists of 615 amino acids with a calculated M(r) of 70,954 and has three coiled-coil domains. Northern and Western blot analyses in mouse tissues indicated that ***ADIP*** was widely distributed. Immunofluorescence and immunoelectron microscopy revealed that ***ADIP*** strictly localized at cell-cell AJs undercoated with F-actin bundles in small intestine absorptive epithelial cells. This localization pattern was the same as those of ***afadin*** and nectin. ***ADIP*** was undetectable at cell-matrix AJs. ***ADIP*** furthermore bound alpha- ***actinin*** , an F-actin-bundling protein known to be indirectly associated with E-cadherin through its direct binding to alpha-catenin. These results indicate that ***ADIP*** is an ***afadin*** - and alpha- ***actinin*** -binding protein that localizes at cell-cell AJs and may have two functions. ***ADIP*** may connect the nectin- ***afadin*** and E-cadherin-catenin systems through alpha- ***actinin*** , and ***ADIP*** may be involved in organization of the actin cytoskeleton at AJs through ***afadin*** and alpha- ***actinin*** .

L3 ANSWER 5 OF 5 JAPIO (C) 2006 JPO on STN
ACCESSION NUMBER: 2004-135658 JAPIO <<LOGINID::20060818>>
TITLE: ***ADIP*** PROTEIN AND USE OF THE SAME
INVENTOR: TAKAI YOSHIMI; IRIE KENJI; ASADA SHIGENORI
PATENT ASSIGNEE(S): EISAI CO LTD
PATENT INFORMATION:

PATENT NO	KIND	DATE	ERA	MAIN IPC
JP 2004135658	A	20040513	Heisei	C12N015-09

APPLICATION INFORMATION
STN FORMAT: JP 2003-293554 20030814
ORIGINAL: JP2003293554 Heisei
PRIORITY APPLN. INFO.: JP 2002-284263 20020927
SOURCE: PATENT ABSTRACTS OF JAPAN (CD-ROM), Unexamined Applications, Vol. 2004
AN 2004-135658 JAPIO <<LOGINID::20060818>>
AB PROBLEM TO BE SOLVED: To provide a new ***afadin*** ***DIL*** ***domain*** - ***binding*** ***protein*** (***ADIP***) gene and a use of the new ***ADIP*** protein.
SOLUTION: This new ***afadin*** -binding protein (***ADIP***) is successfully identified by performing an yeast two hybrid screening in order to obtain an insight in how a nectin and ***afadin*** system organizes a tight junction and an adherence junction in an intercellular junction. The new protein is useful for the evaluation of a medicine for controlling the actin skeleton.

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=> normalization and subtraction of cap-trapper
   4 FILES SEARCHED...
L1            5 NORMALIZATION AND SUBTRACTION OF CAP-TRAPPER

=> dupr em l1
MISSING OPERATOR EM L1
The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

=> dupr rem l1
MISSING OPERATOR REM L1
The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

=> dup rem l1
PROCESSING COMPLETED FOR L1
L2             1 DUP REM L1 (4 DUPLICATES REMOVED)

=> d ibib abs

L2   ANSWER 1 OF 1     MEDLINE on STN                    DUPLICATE 1
ACCESSION NUMBER:   2001084108     MEDLINE <<LOGINID::20060818>>
DOCUMENT NUMBER:    PubMed ID: 11042159
TITLE:                ***Normalization***   and   ***subtraction***
                      ***of***     ***cap***  -  ***trapper***  -selected cDNAs
                    to prepare full-length cDNA libraries for rapid discovery
                    of new genes.
AUTHOR:             Carninci P; Shibata Y; Hayatsu N; Sugahara Y; Shibata K;
                    Itoh M; Konno H; Okazaki Y; Muramatsu M; Hayashizaki Y
CORPORATE SOURCE:   Laboratory for Genome Exploration Research Group, RIKEN
                    Genomic Sciences Center, Tsukuba, Japan..
                    rgscerg@rtc.riken.go.jp
SOURCE:             Genome research, (2000 Oct) Vol. 10, No. 10, pp. 1617-30.
                    Journal code: 9518021. ISSN: 1088-9051.
PUB. COUNTRY:       United States
DOCUMENT TYPE:      Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:           English
FILE SEGMENT:       Priority Journals
ENTRY MONTH:        200101
ENTRY DATE:         Entered STN: 22 Mar 2001
                    Last Updated on STN: 22 Mar 2001
                    Entered Medline: 18 Jan 2001
AB   In the effort to prepare the mouse full-length cDNA encyclopedia, we
     previously developed several techniques to prepare and select full-length
     cDNAs.  To increase the number of different cDNAs, we introduce here a
     strategy to prepare normalized and subtracted cDNA libraries in a single
     step.  The method is based on hybridization of the first-strand,
     full-length cDNA with several RNA drivers, including starting mRNA as the
     normalizing driver and run-off transcripts from minilibraries containing
```

highly expressed genes, rearrayed clones, and previously sequenced cDNAs as subtracting drivers. Our method keeps the proportion of full-length cDNAs in the subtracted/normalized library high. Moreover, our method dramatically enhances the discovery of new genes as compared to results obtained by using standard, full-length cDNA libraries. This procedure can be extended to the preparation of full-length cDNA encyclopedias from other organisms.

```
=> FIL STNGUIDE
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                        ENTRY    SESSION
FULL ESTIMATED COST                                     19.26      19.47

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AND TECHNOLOGY CORPORATION, AND FACHINFORMATIONSZENTRUM KARLSRUHE

FILE CONTAINS CURRENT INFORMATION.
LAST RELOADED: Aug 11, 2006 (20060811/UP).

=> s afadin dil domainbinding protein#
             0 AFADIN
             0 DIL
             0 DOMAINBINDING
             5 PROTEIN#
L3           0 AFADIN DIL DOMAINBINDING PROTEIN#
                 (AFADIN(W)DIL(W)DOMAINBINDING(W)PROTEIN#)

=> s afadin dil domain binding protein#
             0 AFADIN
             0 DIL
             0 DOMAIN
             1 BINDING
             5 PROTEIN#
L4           0 AFADIN DIL DOMAIN BINDING PROTEIN#
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=> s afadin dil domain-binding protein#
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             0 DIL
             0 DOMAIN
             1 BINDING
             5 PROTEIN#
L5           0 AFADIN DIL DOMAIN-BINDING PROTEIN#
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=> s adip
             0 ADIP
L6           0 ADIP

=> s actin#binding protein#
'#' TRUNCATION SYMBOL NOT VALID WITHIN 'ACTIN#BINDING'
The truncation symbol # may be used only at the end of a search term.
To specify a variable character within a word use '!', e.g., 'wom!n'
to search for both 'woman' and 'women'.  Enter "HELP TRUNCATION" at an
arrow prompt (=>) for more information.

=> s actin# binding protein#
             0 ACTIN#
             1 BINDING
             5 PROTEIN#
L7           0 ACTIN# BINDING PROTEIN#
                 (ACTIN#(W)BINDING(W)PROTEIN#)

=> s actin# and binding protein#
             0 ACTIN#
             1 BINDING
             5 PROTEIN#
             0 BINDING PROTEIN#
                 (BINDING(W)PROTEIN#)
```

```
L8            0 ACTIN# AND BINDING PROTEIN#

=> s (actin# and binding) and (protein# or polypeptide#)
              0 ACTIN#
              1 BINDING
              5 PROTEIN#
              0 POLYPEPTIDE#
L9            0 (ACTIN# AND BINDING) AND (PROTEIN# OR POLYPEPTIDE#)

=> s (actinin# and binding) and (protein# or polypeptide#)
              0 ACTININ#
              1 BINDING
              5 PROTEIN#
              0 POLYPEPTIDE#
L10           0 (ACTININ# AND BINDING) AND (PROTEIN# OR POLYPEPTIDE#)

=> s actinin#
L11           0 ACTININ#

=> s actin
              0 ACTIN
L12           0 ACTIN
```